

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 19/526,221
Source: PCT
Date Processed by STIC: 2/27/06

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 02/27/2006

PATENT APPLICATION: US/10/526,221

TIME: 14:37:32

Input Set : A:\265833US0XPCT.ST25.txt

Output Set: N:\CRF4\02272006\J526221.raw

3 <110> APPLICANT: Ferreira, Paulo
 4 Hemerly, Adriana
 6 <120> TITLE OF INVENTION: PLANTS HAVING A CHANGED DEVELOPMENT AND A METHOD FOR MAKING
 THE
 7 SAME
 9 <130> FILE REFERENCE: 265833US0XPCT
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/526,221
 12 <141> CURRENT FILING DATE: 2005-03-01
 14 <150> PRIOR APPLICATION NUMBER: PCT/EP03/10087
 15 <151> PRIOR FILING DATE: 2003-09-05
 17 <150> PRIOR APPLICATION NUMBER: PCT/EP02/10265
 18 <151> PRIOR FILING DATE: 2002-09-05
 20 <160> NUMBER OF SEQ ID NOS: 14
 22 <170> SOFTWARE: PatentIn version 3.3
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 2434
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Arabidopsis thaliana
 29 <400> SEQUENCE: 1

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34	ttgttagcca	ggtgttactt	gagtaacagt	caagcttata	gtgcatatta	tatccttaaa	180
36	ggttcaaaaa	cgcctcagtc	tcggtattta	tttgatttct	catgctttaa	gttggatctt	240
38	cttggagagg	ctgaagctgc	attgttgccc	tgtgaagatt	atgctgaaga	agttcctggt	300
40	ggtgcagctg	ggcatttctt	tcttggctct	atatatagat	attctgggag	gaagaactgt	360
42	tcaatacaac	agtttaggat	ggcattgtca	tttgatccat	tgtgttggga	agcatatgga	420
44	gaactttgta	gttttaggtg	cgcgtgaaga	gcctcaacag	ttttcgggaa	tgttgcttcc	480
46	cagcgtctta	aaacttgtgt	agaacaaaga	ataagcttct	cagaaggagc	aaccatagac	540
48	cagattacag	attctgataa	ggccttaaaa	gatacagggt	tatcgcaaac	agaacacatt	600
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54	caggtaatgg	atgctccacc	gcctctgctt	cttaagaata	tgcgtcgtcc	agcagtggaa	780
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70	cttggagatg	gccacaggca	tttacatatg	tacaagtgtc	aggaagcttt	gttggcatat	1260
72	caaaagctat	ctcagaaaca	atacaataca	cactgggttc	tcatgcagggt	tggaaaagca	1320
74	tattttgagc	tacaagacta	cttcaacgct	gactcttctt	ttactcttgc	tcataaaaag	1380
76	tatctttatg	cttttgaagg	aatggataca	tactccactg	ttctttatca	cctgaaagaa	1440
78	gagatgaggt	tgggctatct	ggctcaggaa	ctgatttcag	ttgatcgctt	gtctccagaa	1500

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84 cacgagtttg cgcatttga agaattcgag gatgcagaga gatgctaccg gaaggctctg 1680
86 ggcatagata cgagacacta taatgcatgg tacgggtcttg gaatgacctt tcttcgtcag 1740
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90 tcagtcatca tgtgttacta tgggaattgct ttgcatgagt caaagagaaa cgatgaggcg 1860
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94 aaggctcaca tattaaccag cctaggtgat tatcacaag cacagaaagt tttagaagag 1980
96 ctcaaagaat gtgctcctca agaaagcagt gtccatgcat cgcttggcaa aatatacaat 2040
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102 ctggtgacgg aggaaaattt gtagatttat tgtgcaggta atacaccaga ttatgtttct 2220
104 catataaccc aaagtcattt gtaatttttc tcatctttag atcagtcttg tggactaacc 2280
106 ctaaaacaaa actgattata taaacttaga gggtaatatt acagaaaatt gtatagagtt 2340
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125 20 25 30
128 Phe Pro Ser Glu Val Asn Leu Gln Leu Leu Ala Arg Cys Tyr Leu Ser
129 35 40 45
132 Asn Ser Gln Ala Tyr Ser Ala Tyr Tyr Ile Leu Lys Gly Ser Lys Thr
133 50 55 60
136 Pro Gln Ser Arg Tyr Leu Phe Ala Phe Ser Cys Phe Lys Leu Asp Leu
137 65 70 75 80
140 Leu Gly Glu Ala Glu Ala Ala Leu Leu Pro Cys Glu Asp Tyr Ala Glu
141 85 90 95
144 Glu Val Pro Gly Gly Ala Ala Gly His Tyr Leu Leu Gly Leu Ile Tyr
145 100 105 110
148 Arg Tyr Ser Gly Arg Lys Asn Cys Ser Ile Gln Gln Phe Arg Met Ala
149 115 120 125
152 Leu Ser Phe Asp Pro Leu Cys Trp Glu Ala Tyr Gly Glu Leu Cys Ser
153 130 135 140
156 Leu Gly Ala Ala Glu Glu Ala Ser Thr Val Phe Gly Asn Val Ala Ser
157 145 150 155 160
160 Gln Arg Leu Gln Lys Thr Cys Val Glu Gln Arg Ile Ser Phe Ser Glu
161 165 170 175
164 Gly Ala Thr Ile Asp Gln Ile Thr Asp Ser Asp Lys Ala Leu Lys Asp
165 180 185 190
168 Thr Gly Leu Ser Gln Thr Glu His Ile Pro Gly Glu Asn Gln Gln Asp
169 195 200 205
172 Leu Lys Ile Met Gln Gln Pro Gly Asp Ile Pro Pro Asn Thr Asp Arg
173 210 215 220

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177 225                230                235                240
180 Leu Gln Val Met Asp Ala Leu Pro Pro Leu Leu Leu Lys Asn Met Arg
181                245                250                255
184 Arg Pro Ala Val Glu Gly Ser Leu Met Ser Val His Gly Val Arg Val
185                260                265                270
188 Arg Arg Arg Asn Phe Phe Ser Glu Glu Leu Ser Ala Glu Ala Gln Glu
189                275                280                285
192 Glu Ser Gly Arg Arg Arg Ser Ala Arg Ile Ala Ala Arg Lys Lys Asn
193                290                295                300
196 Pro Met Ser Gln Ser Phe Gly Lys Asp Ser His Trp Leu His Leu Ser
197 305                310                315                320
200 Pro Ser Glu Ser Asn Tyr Ala Pro Ser Leu Ser Ser Met Ile Gly Lys
201                325                330                335
204 Cys Arg Ile Gln Ser Ser Lys Glu Val Ile Pro Asp Thr Val Thr Leu
205                340                345                350
208 Asn Asp Pro Ala Thr Thr Ser Gly Gln Ser Val Ser Asp Ile Gly Ser
209                355                360                365
212 Ser Val Asp Asp Glu Glu Lys Ser Asn Pro Ser Glu Ser Ser Pro Asp
213                370                375                380
216 Arg Phe Ser Leu Ile Ser Gly Ile Ser Glu Val Leu Ser Leu Leu Lys
217 385                390                395                400
220 Ile Leu Gly Asp Gly His Arg His Leu His Met Tyr Lys Cys Gln Glu
221                405                410                415
224 Ala Leu Leu Ala Tyr Gln Lys Leu Ser Gln Lys Gln Tyr Asn Thr His
225                420                425                430
228 Trp Val Leu Met Gln Val Gly Lys Ala Tyr Phe Glu Leu Gln Asp Tyr
229                435                440                445
232 Phe Asn Ala Asp Ser Ser Phe Thr Leu Ala His Gln Lys Tyr Pro Tyr
233                450                455                460
236 Ala Leu Glu Gly Met Asp Thr Tyr Ser Thr Val Leu Tyr His Leu Lys
237 465                470                475                480
240 Glu Glu Met Arg Leu Gly Tyr Leu Ala Gln Glu Leu Ile Ser Val Asp
241                485                490                495
244 Arg Leu Ser Pro Glu Ser Trp Cys Ala Val Gly Asn Cys Tyr Ser Leu
245                500                505                510
248 Arg Lys Asp His Asp Thr Ala Leu Lys Met Phe Gln Arg Ala Ile Gln
249                515                520                525
252 Leu Asn Glu Arg Phe Thr Tyr Ala His Thr Leu Cys Gly His Glu Phe
253                530                535                540
256 Ala Ala Leu Glu Glu Phe Glu Asp Ala Glu Arg Cys Tyr Arg Lys Ala
257 545                550                555                560
260 Leu Gly Ile Asp Thr Arg His Tyr Asn Ala Trp Tyr Gly Leu Gly Met
261                565                570                575
264 Thr Tyr Leu Arg Gln Glu Lys Phe Glu Phe Ala Gln His Gln Phe Gln
265                580                585                590
268 Leu Ala Leu Gln Ile Asn Pro Arg Ser Ser Val Ile Met Cys Tyr Tyr
269                595                600                605
272 Gly Ile Ala Leu His Glu Ser Lys Arg Asn Asp Glu Ala Leu Met Met

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280 Tyr Lys Ala His Ile Leu Thr Ser Leu Gly Asp Tyr His Lys Ala Gln
281      645      650      655
284 Lys Val Leu Glu Glu Leu Lys Glu Cys Ala Pro Gln Glu Ser Ser Val
285      660      665      670
288 His Ala Ser Leu Gly Lys Ile Tyr Asn Gln Leu Lys Gln Tyr Asp Lys
289      675      680      685
292 Ala Val Leu His Phe Gly Ile Ala Leu Asp Leu Ser Pro Ser Pro Ser
293      690      695      700
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314 ttgttagcca ggtgttactt gagtaacagt caagcttata gtgcatatta tacccttaaa      180
316 ggttcaaaaa cgcctcagtc tcggtattta tttgcattct catgctttta gttggatcct      240
318 cttggagagg ctgaagctgc attgttgccc tgtgaagatt atgctgaaga agttcctggt      300
320 ggtgcagctg ggcattatct tcttgggtctt atatatagat attctgggag gaagaactgt      360
322 tcaatacaac agtttaggat ggcattgtca tttgatccat tgtgttggga agcatatgga      420
324 gaactttgta gtttaggtgc cgtgaagaa gcctcaacag ttttcgggaa tgttgcttcc      480
326 cagcgtctta aaacttgtgt agaacaaaga ataagcttct cagaaggagc aaccatagac      540
328 cagattacag attctgataa ggccttaaaa gatacagggt tatcgcaaac agaacacatt      600
330 ccaggagaga accaacaaga tctgaaaatt atgcagcagc ctggagatat tccaccaa      660
332 actgacaggc aacttagtac aaacggatgg gacttgaaca cacttctcc agtgctttta      720
334 caggtaattg atgctccacc gcctctgctt cttaagaata tgcgtcgtcc agcagtggaa      780
336 ggatctttga tgtctgtaca tggagtgcgt gtgcgtcgaa gaaactttt tagtgaagaa      840
338 ttgtcagcag aggtcaaga agaactctgg cgccgccgta gtgctagaat agcagcaagg      900
340 aaaaagaatc ctatgtcgca gtcatttgga aaagattccc attggttaca tctttcacct      960
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348 tcagaagtgc taagcattct gaaaattctt ggagatggcc acaggcattt acatatgtac      1200
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352 tgggttctca tgcaggttgg aaaagcatat tttgagctac aagactactt caacgctgac      1320
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356 tccactgttc tttatcacct gaaagaagag atgaggttgg gctatctggc tcaggaactg      1440
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368 ctggctctcc aaataaatcc aagatcttca gtcacatgt gttactatgg aattgctttg 1800
370 catgagtcaa agagaaacga tgaggcggtg atgatgatgg agaaggctgt actcactgat 1860
372 gcaaagaatc cgctcccca gttactacaag gtcacatat taaccagcct aggtgattat 1920
374 cacaagcac agaaagtttt agaagagctc aaagaatgtg ctctcaaga aagcagtgtc 1980
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378 ttccggcattg ctttggattt aagcccttct ccatctgatg ctgtcaagat aaaggcttac 2100
380 atggagaggt tgatactacc agacgagctg gtgacggagg aaaatttgta gatttattgt 2160
382 gcaggtaata caccagatta tgtttctcat ataaccctaaa gtcacatctgta atttttctca 2220
384 tcttttagatc agtcttgtgg actaacccta aaacaaaact gattatataa acttagaggg 2280
386 taatattaca gaaaattgta tagagttggg tttgaatttt catttctttt ccaagttgga 2340
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395 <212> TYPE: PRT
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398 <400> SEQUENCE: 4
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405 20 25 30
408 Phe Pro Ser Glu Val Asn Leu Gln Leu Leu Ala Arg Cys Tyr Leu Ser
409 35 40 45
412 Asn Ser Gln Ala Tyr Ser Ala Tyr Tyr Ile Leu Lys Gly Ser Lys Thr
413 50 55 60
416 Pro Gln Ser Arg Tyr Leu Phe Ala Phe Ser Cys Phe Lys Leu Asp Leu
417 65 70 75 80
420 Leu Gly Glu Ala Glu Ala Ala Leu Leu Pro Cys Glu Asp Tyr Ala Glu
421 85 90 95
424 Glu Val Pro Gly Gly Ala Ala Gly His Tyr Leu Leu Gly Leu Ile Tyr
425 100 105 110
428 Arg Tyr Ser Gly Arg Lys Asn Cys Ser Ile Gln Gln Phe Arg Met Ala
429 115 120 125
432 Leu Ser Phe Asp Pro Leu Cys Trp Glu Ala Tyr Gly Glu Leu Cys Ser
433 130 135 140
436 Leu Gly Ala Ala Glu Glu Ala Ser Thr Val Phe Gly Asn Val Ala Ser
437 145 150 155 160
440 Gln Arg Leu Lys Thr Cys Val Glu Gln Arg Ile Ser Phe Ser Glu Gly
441 165 170 175
444 Ala Thr Ile Asp Gln Ile Thr Asp Ser Asp Lys Ala Leu Lys Asp Thr
445 180 185 190
448 Gly Leu Ser Gln Thr Glu His Ile Pro Gly Glu Asn Gln Gln Asp Leu
449 195 200 205
452 Lys Ile Met Gln Gln Pro Gly Asp Ile Pro Pro Asn Thr Asp Arg Gln
453 210 215 220
456 Leu Ser Thr Asn Gly Trp Asp Leu Asn Thr Pro Ser Pro Val Leu Leu
457 225 230 235 240
460 Gln Val Met Asp Ala Pro Pro Pro Leu Leu Lys Asn Met Arg Arg
461 245 250 255

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RAW SEQUENCE LISTING ERROR SUMMARY

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 730,731,732,733 ✓

Seq#:6; Xaa Pos. 244,245

Seq#:7; N Pos. 911,1327,1792

Seq#:8; Xaa Pos. 260,399,554

Seq#:13; N Pos. 26

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:616 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:720
L:730 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:240
L:878 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:900
L:892 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:1320
L:906 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:1740
L:1022 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:256
L:1054 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:384
L:1094 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:544
L:1286 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0